

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 137481

TO: David Lukton

Location: REM-3B75/3C70

Art Unit: 1653

Tuesday, November 16, 2004

Case Serial Number: 09/943002

From: Mary Jane Ruhl

Location: Biotech-Chem Library

Remsen 1-A-62

Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Lukton,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl Technical Information Specialist STIC Remsen 1-A-62 Ext. 22524



SEARCH REQUEST FORM (STIC)

Access DB#	 ;
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Requestor's Name: David Lukton

Examiner number: 71263

Date: 11/9/04

Art Unit: 1653

Phone number: 571-272-0952

Serial Number:

09-943002

Mail Box: 3-C-70

Examiner Rm: 3-B-75

Results format: paper

<u>Title</u>: Novel reovirus-derived proteins and uses therefor

Applicant: Roy Duncan

Earliest Priority Date: 11/7/97

Please search SEQ ID NO: 14

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 15, 2004, 14:47:10 ; Search time 40 Seconds (without alignments) 232.113 Million cell updates/sec

US-09-943-002-14 720 1 MGRHSIVQPPAPPPNAFVE......ERNTRILNHDGRNPDGSINV 140 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

478139 segs, 66318000 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents AA: Database :

/cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ΙD	Description	
1	85	11.8	159	4	US-09-248-796A-16594	Sequence 16594, A	
8	81	11.2	271	4	US-09-252-991A-21522	21522	
m	80.5	11.2	415	4	US-09-710-279-1406	1406,	
4	80.5	11.2	458	m	US-09-134-001C-4663	4663,	
S	75.5	10.5	1220	~	US-08-843-530B-36	36, A	
y	75.5	10.5	1220	4	US-09-636-728-32	32,	
. 7	74	10.3	408	~	US-09-014-969-13	Sequence 13, Appl	
æ	74	10.3	1726	4	US-09-700-227-2	7,7	
σ	74	10.3	1739	4	US-09-540-236-3739	Sequence 3739, Ap	
10	73	10.1	482	4	US-09-328-352-7784	Sequence 7784, Ap	
11	72.5	10.1	338	4	US-09-248-796A-26748	2674	
, 12	72.5	10.1	751	~	US-08-843-530B-32	32,	
13	72.5	10.1	751	4	US-09-636-728-29	29,	
14	71.5	9.9	1257	ო	US-08-611-729A-8	ω,	
15	71.5	6.0	1257	4	US-09-195-524-8	ω`	
16	.71	9.9	174	4	US-09-134-000C-4758	47	
17	70	9.7	507	4	US-09-270-767-44005	440	
18	69	9.6	306	4	US-09-674-529B-2	N	
19	69	9.6	315	4	US-09-674-529B-6	9	
20		9.4	1014	4	US-10-101-464A-807	807	
21	67	9.3	287	4	US-09-543-681A-5282	528	
22	67	9.3	306	4	US-09-674-529B-4	4, Ar	
23	. 67	9.3	309	4	US-09-674-529B-12	12	
24	67	9.3	315	4	US-09-674-529B-8	Sequence 8, Appli	
25	67	9.3	393	4	US-09-248-796A-18493	184	
56	67	6.9	266	4	US-09-543-681A-7802		
27	66.5	9.5	215	4	US-09-248-796A-23074	23074,	

APPLICANT: MAKE J. Rubenfield et al.
APPLICANT: MAKE J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18

•	12893, A	4, Appli	59046, A	2100, Ap	3126, Ap	3152, Ap	5598, Ap	12, Appl	12, Appl	4, Appli	8, Appli	3, Appli	1146, Ap	43662, A	6480, Ap	4, Appli	4, Appli
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-543-681A-6839	US-09-489-039A-12893	US-09-165-396-4	US-09-270-767-59046	US-09-540-236-2100	US-09-710-279-3126	US-09-710-279-3152	US-09-134-001C-5598	US-09-733-524A-12	US-09-092-315-12	US-09-142-551A-4	US-09-390-131-8	US-09-142-551A-3	US-09-538-092-1146	US-09-270-767-43662	US-09-134-000C-6480	US-09-529-279-4	US-10-158-895-4
4	4	4	4	4	4	4	m	4	m	m	4	m	4	4	4	4	4
322	516	799	160	182	238	238	241	355	356	370	393	396	400	795	576	579	579
9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.1	9.1	9.1
66.5	66.5	66.5	99	99	99	99	99	99	99	99	99	99	99	99	65.5	65.5	65.5
28	59	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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Sequence 16594, Application US/09248796A

Sequence 16594, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
FAPPLICATMT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WHORER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION WHORER: US 60/074,725
PRIOR PAPLICATION WHORER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 A-----GVASL------PLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSGTABEN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 FVEIVSSSTGIIIAVGIFAFIFSFL---YKLLOWYNRKSKNKGRKEQIREQIELGLLSYG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
11.8%; Score 85; DB 4;
Best Local Similarity 28.6%; Pred. No. 0.071;
Matches 38; Conservative 14; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-252-991A-21522
; Sequence 21522, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 TRILINHDGRNPDG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 FHLLN----RPEG 143
                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Candida albicans
US-09-248-796A-16594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQIELGLLSYGAGV-ASLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Selitremnikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B FILING DATE: 16-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
11.2%; Score 80.5; DE
Best Local Similarity 34.0%; Pred. No. 1.1;
Matches 17; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Sulte 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.5%; Score 75.5; I 23.3%; Pred. No. 16; tive 22; Mismatches
         CURRENT APPLICATION NUMBER: US/09/134,001C
                                                 CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 4663
LENGTH: 458
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                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/08843530B
Patent No. 5939306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INPORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS: not relevant
not relevant
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INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (415) 705-8410
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Matches 31; Conservative
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STATE: California
COUNTRY: United Stat
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Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:| :|: | | | | : | | : | | : | | : | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 PPPRPPPQRLHSSTGTIMSNVDHABIAKFEALAHRWDRESEBFKPLHD--INPLRVNWID 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 YGAGVASLPLLMVIAHNPGSVISATPIYKGP-CTGVPN-----SRLLQITSGTAEENT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 PPPNAFVBIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKRQIREQIELGLLS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1406, Application US/09710279

Patent No. 6703492

GENERAL INFORMATION:
GENERAL INFORMATION:
MILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PU3480US

CURRENT PELING ADDIES: US/09/710,279

CURRENT PILING DATE: 1999-11-09

PRIOR FILING DATE: 1999-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: | : | |: || : || : || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 || 159 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
11.2%; Score 80.5; DB 4; Length 415;
Best Local Similarity 34.0%; Pred. No. 0.91;
Matches 17; Conservative 13; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.2%; Score 81; DB 4; Length 271; 26.2%; Pred. No. 0.44; tive 25; Mismatches 53; Indels
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FLILMG DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 271
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; NAME/KEY: MOD RES
; LOCATION: (415)
; OTHER INFORMATION: variable amino acid
US-09-710-279-1406
                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 26.2%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 4472
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1406
LENGTH: 415
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US-09-710-279-1406
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IBM PC compatible
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                   US-09-014-969-13
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                       GENERAL INFORMATION:
APPLICANT: Selitrennikoff, Claude
APPLICANT: Selitrennikoff, Claude
APPLICANT: Selitrennikoff, Claude
TITLE OF INVENTION: Histidine Kinases of Aspergillus and Other Fungal
TITLE OF INVENTION: Species, Related Compositions, and Methods of Use
FILE REPERENCE: UTC-0758
CURRENT FILING DATE: 1000-08-09
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 08/843,530
PRIOR PILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver. 2.0
SSO ID NO 32
LENGTH: 1220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LAVALISE, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Recie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Teacy, Multic
APPLICANT: Teacy, Multic
APPLICANT: Agostino, Michael J.
ATILE OF INVENTION: ENCENED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
ADDRESSEE: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.5%; Score 75.5; Di
23.3%; Pred. No. 16;
tive 22; Mismatches
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87 CambridgePark Drive
                                                                                                                                                                                                            Sequence 32, Application US/09636728 Patent No. 6716625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Saccharomyces cerevisiae US-09-636-728-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-014-969-13
; Sequence 13, Application US/09014969
; Patent No. 5965397
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McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                               412 EAGSTTSVSCHGG 424
                                                                           119 TABENTRILINHDG 131
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Best Local Similarity 23.33
Matches 31; Conservative
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412
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61 PAGLESSKRDQSTSMSHINLLFSRRASEPPGPLSVTSHGRPEAPGTKELMSGVHLEMMSP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 VOPPAPPPNAFVEIVSSSTGIIIAV-GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQI
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Sequence 2, Application US/09700227

Patent No. 6706494

GENERAL INFORMATION:
TITLE OF INVENTION: BASB028 Polypeptides and Polynucleotides
TITLE OF INVENTION: Encoding Therefor From Moraxella Catarrhalis
FILE REFERENCE: BM45319

CURRENT APPLICATION NUMBER: US/09/700,227

CURRENT APPLICATION NUMBER: D01-05-14

PRIOR FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GGEGDLHTPMLKLSYSTSQEFSSREELLSCKEEDKSQISFDNLTPSGTL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 ---GVPNSRLLQITSGTA------EBNTRILNHDGRNPDGSI 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 408;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 ----TAEENTRILNHDGR-----NPDGSINV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.3%; Score 74; DB 21.3%; Pred. No. 5.1; tive 32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 AFVELVSSSTGIIIAVGIFAFIFSFL-----
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 498-8284
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                           408 amino acids
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Matches 36; Conservative
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAL
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248, 796A
CURRENT FILING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-06-13
PRIOR PILING DATE: 1998-08-13
SEQ ID NOS: 28208
SEQ ID NOS: 28208
LENGTH: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 IFAIYGCVLFEWATWIANKEYDENEKEETNLAIRKREWAISLAMYLAPSAALFLLAYGAA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 IPAFIFSFLYKLLOWYNRKSKONKKRKEQ----IREQ-----IBLGLLSYGAG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08843530B
Sequence 12, Application US/08843530B
Setent No. 59306
GENERAL INFORMATION:
APPLICANT: Selitrennikoff, Claude
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/843,530B FILING DATE: 16-APP-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
10.1%; Score 72.5; DE
Best Local Similarity 22.8%; Pred. No. 5.8;
Matches 26; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INPORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC
                                                                                                                                                                                                                                                                                                                                                                                                                   Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-248-796A-26748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-08-843-530B-32
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM:
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                                                                                                                        US-09-540-236-3739
US-09-540-236-3739
Sequence 3739, Application US/09540236
Parent No. 6673910
GENERAL INFORMATION: WUCLEIC ALD AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR TITLE OF INVENTION: PULL AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION UNMER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7784, Application US/09328352

Retent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --VLKQNQGK--AGTPVVSQPVSGVQAQR--QIRSGQA 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1494 SPIPVVGDIQGPVBAQTVGDHVFATIGLIPGLGDVAQKAHKAKKAYDTAKSANDVKGMKS 1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 QIREQIELGLLSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSG-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 AFVBIVSSSTGIIIAVGIFAFIFSFL-------YKLLQWYN-RKSKN--KKRKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 PNAF------VEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 EQIBLGLLS-----YGAGVASLPLLNVIAHNPGSVISATPIYKGPCT 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 1739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
10.1%; Score 73; DB 4; Length 482;
Best Local Similarity 30.6%; Pred. No. 8.4;
Matches 34; Conservative 13; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43, Indels
119 ----TABENTRILNHDGR-----NPDGSINV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

10.3%; Score 74; DB
Best Local Similarity 23.5%; Pred. No. 39;
Matches 36; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-09-248-796A-26748
; Sequence 26748, Application US/09248796A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: M.catarrhalis
US-09-540-236-3739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:| ::
1554 AIQEGVD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-195-524-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                  280 PESLAKII---TGTVIAIGVPVILLTL--PLAHW-----AVQPIVRLQKATELITEG 326
                                                                                                                                                                                                            75 AGVASLPLLNVIAHNPGSVISATPIYKGPCTG--VPNSRLLQITSGTAEENTRILNHDGR 132
                                                                                                                                                                                                                                                    ----RASSFKRGFSSGFAVPSS-LLQFNTARAGSTTSVSGHGGS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 PESLAKII---TGTVIAIGVPVILLTL--PLAHW------AVQPIVRLQKATELITEG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 AGVASLPLLNVIAHNPGSVISATPIYKGPCTG--VPNSRLLQITSGTAEENTRILNHDGR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RASSPKRGPSSGFAVPSS-LLÓFNTABAGSTTSVSGHGGS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 PNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIREQIELGLLSYG
                                                                                                                        15 PNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIREQIELGLLSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Selfrennikoff, Claude
APPLICANT: Selfrennikoff, Claude
APPLICANT: Pott, Greg
TITLE OF INVENTION: Histidine Kinases of Aspergillus and Other Fungal
TITLE OF INVENTION: Species, Related Compositions, and Methods of Use
FILE REFERENCE: UTC-03758
CURRENT APPLICATION NUMBER: US/09/636,728
CURRENT PILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 08/843,530
PRIOR APPLICATION NUMBER: 08/843,530
PRIOR APPLICATION NUMBER: 08/843,530
PRIOR SEQ ID NOS: 73
SOFTWARE OF SEQ ID NOS: 73
SOFTWARE Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 751
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10.1%; Score 72.5; DB 4; Length 751;
Best Local Similarity 24.0%; Pred. No. 18;
Matches 31; Conservative 22; Mismatches 43; Indels 3:
                                        Length 751;
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                                     10.1%; Score 72.5; DB 2; 24.0%; Pred. No. 18;
                                                                                22; Mismatches
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Artavania-Tsakonas, Spyridon
Mann, Robert S.
Gray, Grace E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ish-Horowicz, David
Henrique, Domingos M.P.
Lewis, Julian H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT , ORGANISM: Saccharomyces cerevisiae US-09-636-728-29
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Patent No. 6004924
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/09636728
Patent No. 6716625
                               Query Match
Best Local Similarity 24.04
Matches 31, Conservative
                                                                                                                                                                                                                                                    327 RGLS----
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                                                                                                                                                                                                                                                                                              133 -NPDGSINV 140
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TITLE OF INVENTION:
US-08-843-530B-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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48 WYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPG-----SVISATPIY 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.9%; Score 71.5; DB 3; Length 1257; 77.3%; Pred. No. 49; (ve. 18; Mismatches 63; Indels 31.
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CORRESPONDENCE ADDRESS: ADDRESSE: Pennie ADDRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A
FILING DATE: 06-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 7326-037
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 KGPCTGVPNSRLLQITSGTAEENTRILNHDGRNP 134
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NT: Lewis, Julian H.
NT: Lewis, Anna H.
NT: Myat, Anna M.
NT: Pleming, Robert J.
NT: Artavanis-Teakonas, Spyridon
NT: Mann, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 8, Application US/09195524
; Patent No. 6703489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 27.3%;
Matches 42; Conservative 1
                                                                                   1155 Avenue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                      New York
: U.S.A.
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: U.S.A.
                                                                                                                                CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
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Query Match
9.9%; Score 71.5; DB 4; Length 1257;
Best Local Similarity 27.3%; Pred. No. 49;
Matches 42; Conservative 18; Mismatches 63; Indels 31
              MEDIUM TYPE: FLORY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,524
FLING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/195,524
FILING DATE: 06-MAR-1996
ATTORNEY/AGENT INPORMATION:
NAME: MISTOCK, S. Lealie
REGISTRATION NUMBER: 18,872
RESPERENCE/DOCKET NUMBER: 18,872
RESPERENCE/DOCKET NUMBER: 18,872
RELECOMMUTICATION INFORMATION:
TELLEPHONE: (212) 799-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown; MOLECULE TYPE: protein US-09-195-524-8
COMPUTER READABLE FORM:
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48 WYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPG-----SVISATPIY 100 2 GORHSIVOPPAPPNAF-----VBIV---SSSTGIIIAV--GIFAFIFSFLYKLLO 47 989 RRRČPGRPATŘ----PSGRM-RRTRILAAVRŘTP 1017 101 KGPCTGVPNSRLLQITSGTAEENTRILNHDGRNP 134 셤 ઠે ò ઠે

31; Gaps

Search completed: November 15, 2004, 14:59:04 Job time: 42 secs

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November 15, 2004, 14:31:00 ; Search time 155 Seconds (without alignments) 324.014 Million cell updates/sec
                                                                                                                                                                              US-09-943-002-14
720
1 MGRHSIVQPPAPPPNAFVE......EENTRILNHDGRNPDGSINV 140
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                  rotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                    2002273 segs, 358729299 residues
                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
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seq length: 200000000
               Copyright
                                                                                                                                                                                                                                                            BLOSUM62
                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                     Perfect score:
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Maximum DB E
                                                                    OM protein
                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                           Run on:
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geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 23Sep04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*geneseqp2001s:* geneseqp2004s:* Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aay06113 Baboon re	Aau33910 Staphyloc			Abm71462 Staphyloc	Ado25483 Saureus	щ	. Aag82156 S. epider		Abu42716 Protein e			Abb48477 Līsteria	Abu32700 Protein e	Abu26499 Protein e	_	Abb93650 Herbicida	Adk61938 Disease t	Adn07100 S. cerevi		Abr41590 Human DIT	Staphy	c alut	표	Aay45161 Human sec
SUMMARIES	ID	AAY06113	AAU33910	AAU36895	ABU16411	ABM71462	AD025483	AB072776	AAG82156	ABU43432	ABU42716	ABP39818	AD025485	ABB48477	ABU32700	ABU26499	ABG13686	ABB93650	ADK61938	ADN07100	ADJ68848	ABR41590	ABM72920	AAG92924	AAW75856	AAY45161
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	Score	720	84	84	84	84	84	81	80.5	80.5	80.5	80.5	79	78	78	77.5	77	76.5	75.5	75.5	75	74.5	74.5	74.5	74	74
Regult	No.	т	8	e	4	ß	φ	7	80	. .	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aam80143 Human pro Aay57572 Moraxella Ad106053 M. catarr Ad106059 M. catarr		Aab31251 Amino aci Abu31472 Protein e Ada36497 Acinetoba		Aay26968 Wheat Mlo Aab31252 Amino aci Adn07097 S. cerevi	Adp/6092 Arabidops Adm48283 Polypepti Adb64828 Human pro Aab93302 Human pro
AAM80143 AAY57572 ADL06053	ABB61632 AAY26967 AAB01805	AAB31251 ABU31472 ADA36497	ADH71860 ABG96273 ADH71856	AAY26968 AAB31252 ADN07097	ADP76092 ADM48283 ADB64828 AAB93302
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1455 1726 1739	534 534 534 534	534 262 482	543 766 766	534 534 751	1677 649 687 775
10.3	10.22	10.5	 	20.1	100.0
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25 28 28 28	3310	33 34 54	3 3 4 6 8 5 6 8 5 6 8 5 6 8 5 6 8 5 6 8 5 6 6 6 6	0 4 4 0 0 ti	4 4 4 4 2 6 4 0

ALIGNMENTS

Orthoreovirus; reovirus; BRV; P15 protein; fusogenic protein; cell fusion; membrane fusion; syncytium formation. 27. .41
/note= "transmembrane domain" Baboon reovirus fusogenic protein P15a. Location/Qualifiers AAY06113 standard; protein; 140 AA. (first entry) Baboon reovirus. 16-AUG-1999 AAY06113, Key Domain RESULT 1 AAY06113

98WO-CA001046. WO9924582-A1. 06-NOV-1998; 20-MAY-1999.

97US-00965708.

07-NOV-1997;

(UYDA-) UNIV DALHOUSIE,

WPI; 1999-327410/27. N-PSDB; AAX58670. Juncan R;

Fusogenic proteins from non-enveloped reoviruses.

Example 6; Page 53-54; 57pp; English.

The present sequence represents the fusogenic protein P15a of baboon recovirus (BRV). 2 Unrelated fusion proteins responsible for cell-cell fusion induced by avian recovirus (ARV) and the only 2 fusogenic mammalian recoviruses, Nelson Bay virus (NBV) and BRV, are identified in this invention. These proteins are termed P11 for ARV and NBV (see also AAV66104, AAV66107 and AAV66110) and P15 for BRV. Fusogenic P11 and P15 are useful for (1) promoting fusion of cell, liposome or proteoliposome membranes; production of B and T cell hybridomas or other heterokaryons (they eliminate the need to use toxic chemicals such as PBG); (111) for producing fusions between liposomes and cells or other liposomes; and

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(iv) for incorporation into liposomes to allow intra- or extracellular delivery of bioactive agents (e.g. nucleic acid, proteins and metabolic regulators), both in vivo and in cell cultures. Antibodies raised against Pil or Pis are useful for diagnosis and therapeutically (e.g. to block undestrable fusion processes). Pil and Pis are smaller than fusogenic proteins from enveloped viruses and are not glycosylated, so are essier to produce and purify using recombinant expression systems. They do not require a signal peptide for membrane entry, are not immunogenic and are functional at neutral ph
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                                                                                                                                                                                                                                                                                                                       MGQRHSIVQPPAPPPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKKKE
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                                                                                                                                                                                                     Sequence 140 AA;
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Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                         Staphylococcus aureus cellular proliferation protein #186.
          AAU33910 standard; protein; 431 AA
                               14-FEB-2002 (first entry)
                                                                    Staphylococcus aureus
                                                                              WO200170955-A2
                    AAU33910;
     AAU33910
RESULT
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2000US-0253625P. 2000US-0257931P. 2001US-0269308P. 2000US-0206848P. 2000US-0207727P. 21-MAR-2001, 2001WO-US009180 2000US-0191078P 2000US-0242578P 23-OCT-2000; 27-NOV-2000; 22-DEC-2000; 16-FEB-2001; 21-MAR-2000; 23-MAY-2000; 26-MAY-2000; 27-SEP-2001

(ELIT-) ELITRA PHARM INC

Haselbeck R,

New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids. Ohlsen KL, Xu HH; WPI; 2001-611495/70. N-PSDB; AAS51769. Yamamoto RT,

Carr Si

Trawick JD,

Wall D,

Zyskind JW,

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, Example 3, SEQ ID NO 5406; 511pp; English.

themselves and the encoded proteins. The prokaryotes used are Bacherichia coli, Staphylococcus aureus, Salmonella typhi Klebsiella pneumoniae, con the interpretary of greatella in invention is also useful for the identification of potential new targets for antibiotic con useful for the antisense mucleic acids can also be used to identify contribodies capable of binding to the expressed proteins. The proteins can entisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in clerwipo int/pub/published_pot_sequences 33 GIFAFIFSFLYKLLOWYNRKSKNKKKEQIREQIBLGLLSYGAGVASLPLLNVIAHNPGS Carr GJ; 22; Gaps use in the discovery of novel antibiotics, the essential genes Antisense, prokaryotic cellular proliferation protein, antibiotic, antibacterial, drug design. New polynucleotides for the identification and development of antiblotics, comprise sequences of antisense nucleic acids. Trawick JD, Staphylococcus aureus cellular proliferation protein #1065. 11.7%; Score 84; DB 4; Length 431; 26.5%; Pred. No. 2.2; sive 15; Mismatches 35; Indels 93 VISATPIYKGPCTGVPNSRLLQITSGTABENTRILNHD 130 194 IBSYVCKHLG-----IGTAPVSTOTLORD 217 Zyskind JW, Wall D, Example 3; SEQ ID NO 12488; 511pp; English Ź AAU36895 standard; protein; 431 2000US-0191078P. 2000US-0206848P. 2000US-0207727P. 2000US-0242578P. 21-MAR-2001; 2001WO-US009180 2000US-0253625P 2000US-0257931P 2001US-0269308P (first entry) 26, Conservative (ELIT-) ELITRA PHARM INC. Ohlsen KL, Staphylococcus aureus Xu HH; WPI; 2001-611495/70. N-PSDB; AAS54754. Similarity WO200170955-A2 16-FEB-2001; 23-MAY-2000; 27-NOV-2000; 22-DEC-2000; Haselbeck R, Yamamoto RT, 21-MAR-2000; 26-MAY-2000; 3-OCT-2000; 14-FEB-2002 27-SEP-2001 AAU36895; Query Match Best Local 9 Matches RESULT 3 AAU36895 85888888888888888888 ઠ 名 ઠે ద

Claim 25; SEQ ID NO 44335; 1766pp; English.

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antiblotics, the essential genes chemical the discovery of novel antiblotics, the essential genes chemical and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, seruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antiblotic development. The antisense nucleic acids can also be used to identify contents used in proliferation, to express these protesins. The proteins antisense nucleic acids esquence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in clearing the problished_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 GIFAFIFSFLYKLLQWYNRKSKNKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGS 92
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Xu HH;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #1938.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 IBSYVCKHLG-----IGTAPVSTQTLQRD 217
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Yamamoto R,
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Carr GJ,
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06-SEP-2001, 2001US-0094893.
25-OCT-2001, 2001US-0342921P.
08-FEB-2002, 2002US-00072851.
06-MAR-2002, 2002US-0362699P.
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Best Local Similarity 26.54
Matches 26; Conservative
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Trawick JD,
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N-PSDB; ACA20281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 431 AA;
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Wall D,
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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
to the muclaic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
condition acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting callular
proliferation or the activity of a gene in an operon required for
proliferation or the activity of agene in an operon required for
the gene product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the con-
product is overaxpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits for
conjecution of an organism. The antisense nucleic acids required
the colligration of an organism or solution and all and acids required
to reduct its overaxpressed or solution and antisense nucleic acids required
to religious proteins or screening for homologous nucleic acids required
to reduct the colliferation of an organism. The antisense mucleic acids required
to require the colliferation of an organism or solution and antisense nucleic acids required
to require the colliferation or for solute condition and acids required
to required to reference the cond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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Local Similarity 26.5%; Pred. No. 2.2;
es 26; Conservative 15; Mismatches
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Matches
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ABM71462
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(CHIR-) CHIRON SPA

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                                                                                                                            Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
                                                                                                                                                                                                                                                                                                                    ----TFANIPPE 216
                                                         New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                                 33 GIFAFIPSFLYKLLQWYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGS 92
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                              22;
                                                                                                                       The invention relates to novel genes and encoded proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antimicrobial, microbial disease; drug composition; vaccine; bacterial infection; antibacterial; food preservative.
                                                                                                                                                                                                                                                       11.7%; Score 84; DB 6; Length 454; 26.5%; Pred. No. 2.3; ive 15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                             165 GVHAEPTTFGVKMALMYTEMQRNLQRFKQVREEIEVGKMSGAVG-
                                                                                                                                                                                                                                                                                                                                         93 VISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHD 130
                                                                                                                                                                                                                                                                                                                                                      217 IBSYVCKHLG------IGTAPUSTQTLQRD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S_aureus adenylosuccinate lyase purB protein Seq158.
                                                                                                  Claim 1, SEQ ID NO 1404; 49pp; English.
         Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                               ADO25483 standard; protein; 454 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002US-0423757P.
2002US-0423758P.
2002US-0423791P.
2002US-0423832P.
2002US-0423875P.
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2002US-0424502P
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                                                                                                                                                                                                                                                                   Local Similarity 26.5
nes 26; Conservative
         Masignani V, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus
                            WPI; 2003-120786/11.
                                       N-PSDB; ACP73022
                                                                                                                                                                                                                                      Sequence 454 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004041854-A2
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07-NOV-2002;
07-NOV-2002;
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05-NOV-2002;
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05-NOV-2002;
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06-NOV-2002;
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05-NOV-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AD025483;
                                                                                                                                                                                                                                                         Query Match
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ADO25483
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This invention relates to the identification of novel protein targets for the development of antimicrobial drugs against pathogenic bacteria. Specifically, it refers to recombinant proteins derived from Staphylococcus aureus, Helicobacter pylori, Streptococcus paumoniae, Bacherichia coli, Enterococcus faecalis or Pseudomonas aeruginosa. The present invention describes providing a three-dimensional structure for these crystallised proteins to identify a potential modulator for the prevention or treatment of microbial diseases. Purthermore, contacting a protein with a modulator can be useful for assaying protein activity and hence its viability in drug composition or vaccine. Accordingly, such compositions can be useful for treating bacterial infections, developing antibacterial agents useful as food preservatives or treating food products to eliminate potential pathogens. This polypeptide sequence is a bacterial protein target of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacterial polypeptide composition useful for treating bacterial infection, has isolated, recombinant bacterial polypeptide such as GTP-binding protein Era from Pseudomonas aeruginosa or adenylosuccinate lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLENVIAHNPGS 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 84; DB 8; Length 454; 26.5%; Pred. No. 2.3; ive 15; Mismatches 35; Indels
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Ng I, Virag C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 41; SEQ ID NO 158; 566pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vedadi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alam MZ,
                                                        2002US-0425118P.
2002US-0425126P.
2002US-0425162P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 26.5*
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 00308-045501
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Buzadzija K;
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08-NOV-2002;
08-NOV-2002;
08-NOV-2002;
08-NOV-2002;
08-NOV-2002;
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Mansoury K,
Mcdonald M,
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Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;

Staphylococcus epidermidis.

endocarditis.

09-NOV-2000; 2000WO-US030782

17-MAY-2001.

epidermidia open reading frame protein sequence SEQ ID NO:1406.

(first entry)

03-SEP-2001

AAG82156;

AAG82156 standard, protein, 415 AA.

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The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as templates for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa sequences of Pseudomonas species using biochip technology. Sequences ABO67826-components for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid encoding Peeudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPPNAFVBIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIREQIELGLLS 72
                                                                                                                                                               Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.2%; Score 81; DB 7; Length 271; 26.2%; Pred. No. 2.6; ive 25; Mismatches 53; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                Deloughery C,
                                                                                                                                Pseudomonas aeruginosa polypeptide #4951.
                             AB072776 standard; protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                              98US-0074788P.
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                                                                                               (first entry)
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                                                                                                                                                                                               Pseudomonas aeruginosa.
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N-PSDB; ABD06347.
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                                                                                                                                                                                                                                                                                                                                                                                                              Rubenfield MJ,
                                                                                                                                                                                                                                                                                               .8-FEB-1999;
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                                                                                               29-JUL-2004
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Best Local Si
Matches 32,
                                                               AB072776;
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RESULT
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Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.

WPI; 2001-316495/33.

Kimmerly WJ;

N-PSDB; AAH53006

(GLAX) GLAXO GROUP

09-NOV-1999;

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(II), given in AAG81155. Interest and the control of properties and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the 8.

epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts calls which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their cativity and therefore identify compounds that may be used for the treatment of 8. epidermidis infections, e.g. endocarditis AAH53091 to AAH55090 represent opposities infections, e.g. endocarditis AAH53091 to AAH55090 represent oligonucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences are nin the exemplification of the present invention. N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence is not the present specification. In the disclosure for SEQ ID NO:4465 to even though sequences are present in the control of the present specification of the present specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 397-398; 2188pp; English.
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les 17; Conserva
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Matches
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AC ABU4
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19-JUN-2003 (first entry)
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Best Local Similarity 34.0%
Matches 17; Conservative
                                                       N-PSDB; ACA47302
                                                                                                                                              Sequence 431 AA;
                 WO200277183-A2.
                     03-OCT-2002.
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                                               Wang |
Wall |
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WO200277183-A2
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(1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a nost cell containing the vector; (3) an isolated or polypeptide cid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway cequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; activity; (11) a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the culture or collection of strains; or (13) identifying the target of a compound that inhibits the contained for proliferation of an organism. The antisense nucleic acids are useful for deriving an organism contains and activity; (10) activity of the strains of a compound that inhibits are lighted for cellular proliferation to several activity of a compound that inhibits are lighted for cellular proliferation to several activity of a compound that inhibits are lighted for cellular proliferation to several activity of a several activity 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at figure.
                                                                                                                                       Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen KL,
Forsyth RA,
                                             Protein encoded by Prokaryotic essential gene #28959.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 71356; 1766pp; English.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-03429228-
08-FEB-2002; 2002US-0072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                      Staphylococcus haemolyticus
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Trawick JD,
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The invention relates to an inclusion and where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated contained by the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular containing a compound that influences the activity of the polypeptide; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway to that has an activity against a biological pathway in which a proliferation required for cellular proliferation of incompound a activity; (1) a culture complication or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits the product is overexpressed or underexpressed; (12) determining the extent compound; activity; (11) a culture complishing strains in which had not should be activity; (11) a culture complishing strains in conflection of the present of a compound that inhibits the product is overexpressed or underexpressed; (12) determining the extent of the present in a culture or collection of conflection of the present of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for danged discovery programs, or for screening for homologous nucleic acids are useful of the proliferation to isolate candidate modeled for proliferation in collections. The sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening
                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid comprising any
Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #28243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 70640; 1766pp; English
                                                                                                                                         ABU42716 standard, protein, 431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-2002; 2002US-00072851.
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25-OCT-2001; 2001US-0342923P.
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                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis.
                                                                                                                                                                                                                              (first entry)
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Trawick JD,
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N-PSDB; ACA46586.
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11.2%; Score 80.5; DE 34.0%; Pred. No. 5.4; tive 13; Mismatches

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Gaps

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19; Indels

DB 6; Length 431;

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antimicrobial; microbial disease; drug composition; vaccine;
bacterial infection; antibacterial; food preservative.
                                                                                                                                                                                                                    S_aureus adenylosuccinate lyase purB protein Seq160.
                             ADO25485 standard; protein; 454 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-2003; 2003WO-CA001671.
                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004041854-A2
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05-NOV-2002;
                                                                                                                                                      12-AUG-2004
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                                                                                           AD025485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200
   AD025485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in open therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to incerfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4663.
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                                                                                                                                                         Length 431;
                                                                                                                                                                                                                                                                                  33 GIFAFIFSFLYKLLQWYNRKSKNKKRKEQIREQIELGLLSYGAGV-ASLP
                                                                                                                                                                                                             19; Indels
                                                                                                                                                         9
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; Pred. No. 5.4;
13; Mismatches
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in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP39818 standard, protein, 458
                                                                                                                                                      11.2%;
34.0%;
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                                                                                                                     Query Match
Best Local Similarity 34.0.
These 17; Conservative
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N-PSDB; ABN92363.
                                                                                           Sequence 431 AA;
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08-NOV-1997;
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ABP39818
XX ABP39
XX ABP39
XX ABP39
XX XX Staph
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Bacterial polypeptide composition useful for treating bacterial infection, has isolated, recombinant bacterial polypeptide such as GTP-
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Alam MZ, Ng I, Virag C, Houston S;
                                                                                                                                                           003US-0455334P
003US-0455335P
                                              US-0454193P
                                                      US-0454215P
                                                               003US-0454218P
                                                                                           003US-0454536P
                                                                                                              003US-0455036P
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                                                                                                                                                                                                 (AFFI-) AFFINIUM PHARM INC.
                                                                         003US-045448
                                                                                                                                                                                                                                     Buzadzija K;
        002US-04252
                                                                                                                                                                                                                    Dharamsi A,
US-0425
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                                                                                                                                                                                                                                                        WPI; 2004-400642/37.
N-PSDB; ADO25484.
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Mansoury K,
Mcdonald M,
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Gaps

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GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQIELGLLSYGAGV-ASLP 81

Local Similarity 34.04 tes 17; Conservative

Best Loc Matches

33 169

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RESULT 12

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This invention relates to the identification of novel protein targets for the development of antimicrobial drugs against pathogenic bacteria. Specifically, it refers to recombinant proteins derived from Staphylococcus aureus, Helicobacter pylori, Streptococcus pneumoniae, Bscherichia coli, Enterococcus faecalis or Pseudomonas aeruginosa. The present invention describes providing a three-dimensional structure for these crystallised proteins to identify a potential modulator for the prevention or treatment of microbial diseases. Furthermore, contacting a protein with a modulator can be useful for assaying protein activity and hence its viability in drug composition or vaccine. Accordingly, such compositions can be useful for treating bacterial infections, developing antibacterial agents useful as food preservatives or treating food products to eliminate potential pathogens. This polypeptide sequence is a bacterial protein target of the invention.
protein Bra from Pseudomonas aeruginosa or adenylosuccinate lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TFANIPPE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 GIFAFIFSFLYKILQWYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dussurget C, rrangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng B, Vazquez-Boland JA, Dominguez-Bernal G, Garrido-García P, Tierrez-Martinez A, Amend A Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L, Perez-Diaz J, Baquero F, García Del Portillo F, Gomez-Lopez N; Anduenio B, De Pablos B, Wehland J, Kaerst U, Entian K Haner T, Rose M, Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                     11.0%; Score 79; DB 8; Length 454; 25.5%; Pred. No. 8.6; ive 16; Mismatches 35; Indels
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                                                       Claim 41; SEQ ID NO 160; 566pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeria monocytogenes protein #1181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB48477 standard; protein; 391 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2000; 2000FR-00004629
                   from Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 IESYVCKHLG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                Sequence 454 AA;
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Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related

WPI; 2002-010914/01.

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The present invention relates to the genome sequence of Listeria

monocytogenes EGD-e (see ABA3041). The genome sequence and fragments of

it are useful for selecting probes and primers for detecting genes in L.

concock to the genome sequence and for studying genetic

polymorphisms and other genomes. The present sequence is a protein

concock by the genome sequence are useful for raising specific

expressed from the genome sequence are useful for raising specific

contibodies, identification of L. monocytogenes and related organisms, and

for blooynthesis and biodegradation, especially biosynthesis of Vitamin

CC antibodies, identification of L. monocytogenes and related organisms, and

for blooynthesis and biodegradation, especially biosynthesis of Vitamin

CC antibodies in monocytogenes-related diseases. In addition, the genome

cand modulate L. monocytogenes-related diseases. In addition, the genome

cequence and proteins encoded by it are useful in pharmaceutical and

vaccines compositions for the treatment or prevention of infections by L.

connocytogenes and related organisms. Note: The sequence data for this

connocytogenes and related organisms. Note: The sequence data for this

connocytogenes and related organisms. Note: The sequence data for this

connocytogenes and related organisms. Note: The sequence data for this

connocytogenes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 KKAAEESREQIEEALKGSDMVFVTAGMGGGTGTGAAPVIAQIAKEMGALTVGVVTRPFGF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38; Gaps
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 KGP-----CTG-----VPNSRLLQITSGTABENTRIL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%; Score 78; DB 5; Length 391; 28.3%; Pred. No. 9.1; ive 14; Mismatches 24; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #18227.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                     Claim 6; SEQ ID NO 1182, 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU32700 standard; protein; 391 AA
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Carr GJ,
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06-SBP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2002; 2002WO-US009107.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-029926/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 391 AA;
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25-OCT-2001;
08-FEB-2002;
polypeptides
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Wall D,
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Matches
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the international control of a cell. Also included are:

(1) a vector comprising proliferation of a cell. Also included are:

(1) a vector comprising a promiter of a cell. Also included are:

(1) a vector comprising a promiter operably linked to the nucleic acid

encoding a polypeptide whose expression is inhibited by the antisense

nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC plypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (6) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of required for proliferation, or that inhibite cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway or a gene or which the test compound that inhibite proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that compound that inhibite stend of the strains is present in a culture or collection of compound a activity; (11) a culture comprising strains in which the gene product is overexpressed or undersexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of proliferation of an organism. The antisense nucleic acids are useful for electing proteins or screening for homologous nucleic acids required for election or for exceening for homologous nucleic acids required for election or for exceening for homologous nucleic acids required for election or for exceening for homologous nucleic acids required for and decomposition or an organism and provention or an organism and provention or an organism and proventions and acids are useful for election or for exceening for homologous nucleic acids required for an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, R. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
      homologous nucleic acids required for cellular proliferation to
                              isolate candidate molecules for rational drug discovery programs.
                                                                                                Claim 25; SEQ ID NO 60624; 1766pp; English.
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KKRKEQIREQIELGL-----LSYGAGVASLPLLINVIAHNPGS----VISATPIY 100 79 KKAAEESKEQIEEALKGSDMVFVTAGMGGGTGTGAAPVIAQIAKEMGALTVGVVTRPFGF 138 101 KGP-----CTG------VPNSRLLQITSGTABENTRIL 127 10.8%; Score 78; DB 6; Length 391; 28.3%; Pred. No. 9.1; ive 14; Mismatches 24; Indels Best Local Similarity 28.3%; Matches 30; Conservative 1

Gaps

38;

ABU26499 standard, protein; 339 AA 19-JUN-2003 (first entry) ABU26499;

Protein encoded by Prokaryotic essential gene #12026.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Campylobacter jejuni

WO200277183-A2.

03-OCT-2002.

21-MAR-2002, 2002WO-US009107

21-MAR-2001, 2001US-00815242

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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
co the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
concoling a polypeptide whose expression is inhibited by the antisense
concoling a polypeptide whose expression is inhibited by the antisense
concoling a cid, (4) an antibody capable of specifically binding
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid, (4) an antibody capable of specifically binding
colliferation or the activity of agene in an operon required for
proliferation or the activity of agene in an operon required for
concline product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene product is agene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound's activity; (12) dentifying a culture acide required
compound's activity; (12) a dentifying the target of a compound that inhibits the
compound are activity of an organism. The antisense nucleic acide are useful for
dentifying proteins or screening for homologous nucleic acide required
conditional proliferation of solution of an organism and activity and antisense of a compound and activity activity and activity activity
                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                       Zyskind JW;
Xu HH;
                                                                                                                                                                                          Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                          Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 54423; 1766pp; English.
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                                                                                                                                                                                          Malone C,
                                                                                                                                                                                                                       Carr GJ,
                    25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                    ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                       Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                            WPI; 2003-029926/02.
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                                                                                                                                                                                          Wang L,
Wall D,
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Sequence 339 AA;

61 WILDKEKNIILQNQEALKNPKLLSIISLDKIRDELBFBGRFYA------VKIIAHNBK 112 48 WYNRKSKN-----KKRK-----EQIREQIELGLLSYGAGVASLPLLINVIAHNPG 91 33; Gaps 92 SVISATPIYKGPCTGVPNSRLLQITSGTABENTRILNHDGRNPDGSINV 140 113 IIVSATDI----SDEKRNERLASMGSVAAH-----LAHEIRNPIGSISL 152 Length 339; 10.8%; Score 77.5; DB 6; Length 3 28.4%; Pred. No. 8.6; ive 14; Mismatches 31; Indels 31; Conservative Best Local Similarity Query Match Matches

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Search completed: November 15, 2004, 14:54:18 Job time : 164 secs

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-09-943-002-14
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Sequence 45755, A
Sequence 9226, Ap
Sequence 70640, A
Sequence 200688,
Sequence 29701, A
Sequence 29480,
Sequence 18328, A
Sequence 18328,
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290480,
43526, A
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Sequence 5406, Ap
Sequence 12488, A
                                                                                 (without alignments)
351.310 Million cell updates/sec
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                                                                       ; Search time 141 Seconds
                                                                                                                                            1 MGQRHSIVQPPAPPPNAFVE......EENTRILINHDGRNPDGSINV
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Compugen Ltd
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US-09-815-242-5406
US-09-815-242-12488
US-09-815-242-12488
US-00-10-283-122A-44335
US-10-739-930-8926
US-10-739-930-8926
US-10-739-930-8926
US-10-739-930-8926
US-10-739-930-8926
US-10-424-599-200688
US-10-425-114-33701
US-10-425-114-33568
                                                                                                                                                                                                                                 hits satisfying chosen parameters:
                                                                                                                                                                                                          1568699 segs, 353819137 residues
GenCore version (c) 1993 - 2004
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                                                                     November 15, 2004, 14:51:55
                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                              Published_Applications_AA:
                                               - protein search, using sw model
                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
           Copyright
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Sequence 54423, A Sequence 54999, A Sequence 312, App Sequence 12082, A Sequence 51999, A Sequence 51999, A Sequence 654, App Sequence 6678, App Sequence 1998, A Sequence 31269, Sequence 312699, Sequence 11, Appl Sequence 274608, Sequence 214608, Sequence 214608, Sequence 21666, Sequence 2982, App Sequence 2982, App Sequence 2982, App Sequence 2982, App Sequence 10089, Sequence 2982, App Sequence 2982, App Sequence 2666, Sequence 2666, Sequence 2666, Sequence 2666, Sequence 3051, App Sequence 2666, Sequence 2666, Sequence 2666, Sequence 3051, App Sequence 2666, Sequence 3051, App Sequence 2666, Sequence 3051, App Sequence 3051, App Sequence 2666, Sequence 3051, App Sequ
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158433,
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4 US-10-369-493-10884

US-10-282-122A-66624

US-10-425-114-54929

US-10-425-114-54929

US-09-10-369-493-5059

US-09-10-369-493-5059

US-09-10-493-149924

US-10-425-114-53999

US-10-425-114-518924

US-10-425-114-518924

US-10-425-114-41480

US-10-425-115-305682

US-10-425-115-305682

US-10-425-115-305682

US-10-425-115-305682

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US-10-425-115-30582

US-10-425-115-30582

US-10-425-115-30582

US-10-425-115-30895

US-10-437-963-150666

US-10-368-421-8

US-10-368-421-8
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US-10-437-963-142238
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ALIGNMENTS

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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QIREQIELGLESYGAGVASLPLINVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                                                                           APPLICANT: Duncan, Roy
TITLE OF INVENTION: NOVEL REOVIRUS-DERIVED PROTEINS AND USES THEREFOR
FILE REFERENCE: 78973-1C
CURRENT APPLICATION NUMBER: US/09/943,002
CURRENT PELLING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PEASESEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 140
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 140;
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Sequence 14, Application US/09943002
Patent No. US20020045734A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 EENTRILNHDGRNPDGSINV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
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                                                                                                                                                                                                                                                                                                                            ORGANISM: baboon reovirus US-09-943-002-14
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33 GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGS 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 11.7%; Score 84; DB 9
1 Similarity 26.5%; Pred. No. 2.1;
26; Conservative 15; Mismatches
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR PRIOR DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FREUSEQ FOR WINDOWS Version 4.0
SEQ ID NO 12488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44335, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FIGURE DATE: 2003-02-02 CURRENT FILING DATE: 2003-02-02 CURRENT FILING DATE: 2003-02-02 CURRENT FILING DATE: 2000-03-10-03 ENGINE APPLICATION NUMBER: 60/206, 848 PRIOR FILING DATE: 2000-05-25 PRIOR PELICATION NUMBER: 60/207, 727 PRIOR PELICATION NUMBER: 60/207, 727 PRIOR PILING DATE: 2000-09-06 ENGINE PILING DATE: 2000-09-09 ENGINE PILING DATE: 2000-10-23 ENGINE APPLICATION NUMBER: 60/242, 578 PRIOR PILING DATE: 2000-10-23 ENGINE PILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12488
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Forsyth, R.
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Best Local S
Matches 26
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APPLICANT: Tradick, John D.
APPLICANT: Tradick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prockaryctes
TITLE OF INVENTION: Prockaryctes
TITLE OF INVENTION: Prockaryctes
TILLE OF INVENTION: PROCKARYCTES
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILLING DATE: 2000-03-21
PRIOR PILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-10-23
PRIOR PILLING DATE: 2000-110-23
PRIOR PILLING DATE: 2000-110-23
PRIOR PILLING DATE: 2000-112-22
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APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard: T.
IITLE OF INVENTION: Identification of Essential Genes in IITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 VISATPIYKGPCTGVPNSRLLQITSGTABENTRILNHD 130
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11.7%; Score 84; DB 5
Best Local Similarity 26.5%; Pred. No. 2.1;
Matches 26; Conservative 15; Mismatches
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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Patent No. US20020061569A1
          Sequence 5406, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5406
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Zyskind, Judith W.
Wall, Daniel
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22; Gaps

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-10-282-122A-70640
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ORGANISM:
                                                                                                                                                                     FEATURE:
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APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: As and Weleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
MUMBER OF SEQ ID NOS: 73128

LENGTH: 636
TYPE: pro-
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TITLE OP INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OP INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53377) B
                                                                                                                                                                                                                                                                                                                                                142 GVHAEPTIFGVKMALWYTEMQRNLQRPKQVREBIBVGKMSGAVG-----IFANIPPE 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 HAAAAAPGPAPNHINKHKHSKRKLLGWILGFVAGALGGTLSGFVFSLMFKLALALIKGRG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 ŘKAGPDIYSPLÍKKAEDĽAFĽEKBEGIÁŠĽEIIGRGGCGBVYKÁELPĠŠNGKMÍAIKKÍV 375
                                                                                                                                                                                                                                                                                                         33 GIFAFIPSFLYKLLQWYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGS 92
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                                                                                                                                                                                                                                                            Gaps
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: Patentin version 3.1 SEQ ID NO 44335 LENGTH: 431
                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64; Indels 34;
                                                                                                                                                                                                            ; Score 84; DB 15; Length 431;
; Pred. No. 2.1;
15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.7%; Score 84; DB 15; Length 636; 22.0%; Pred. No. 3.5; tive 26; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 KGPCTGVPNSRLLQITSGTAEBNTRILNHDGRNPDGSIN 139
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                                                                                                                                                                                                                                                                                                                                                                                                  93 VISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: 700834446_FLI.pep
US-10-425-114-45755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8926, Application US/10739930 Publication No. US20040216190A1 GENERAL INFORMATION:
                                                                                                              TYPE: PRT CAGANISM: Staphylococcus aureus US-10-282-122A-44335
                                                                                                                                                                                                         Query Match
Best Local Similarity 26.5%;
Matches 26; Conservative 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 22.0*
Marches 35; Conservative
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ORGANISM: Glycine max
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280 ÓPPSPPPPPAAVVPKESKSSNKVGVÍVGSVLGGFAFLVLLSLÍVLMLLKYKOKKKIQÓME 339
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                                                                                                                                                                                                                                                                                                  11.2%; Score 80.5; DB 17; Length 376; 29.7%; Pred. No. 4.3; tive 12; Mismatches 35; Indels 5
                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: GLYMA-23APR03-C245578_1.p
US-10-739-930-8926
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CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 8926
LENGTH: 376
TYPE: PRT
ORGANISM: Glycine max
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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Publication No. US20040029129A1
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
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PPLICANT: Zamudio, Carlos
Malone, Cherryl
PPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 EQIELGLLSYGAGV 77
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Yamamoto, Robert
Forsyth, R.
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , John
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Trawick, Joh
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2000-03-02-03
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/200,848
PRIOR APPLICATION NUMBER: 60/200,848
PRIOR APPLICATION NUMBER: 60/200,335
PRIOR APPLICATION NUMBER: 60/200,335
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
                                                                 Gaps
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                                                                                                                        142 GVHAEPTTFGVKMALMYTEMKRNLKRPKEVRKEIEVGKMSGAVGTFANIP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQIBLGLLSYGAGV-ASLP 81
   Length 431;
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         DB 15;
Query Match
11.2%; Score 80.5; DE
Best Local Similarity 34.0%; Pred. No. 5.1;
Matches 17; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                        Sequence 71356, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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; Sequence 200688, Application US/10424599
; Publication No. US20040031072A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Hagelbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Lou, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: 1003-04-28
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
TYPE: DENGTH: 760
                                                                                                                        Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 KPTARPTNDGTNSMSSNNTPSHSGGLSTGGSVAIGIVVGPIVLSLLVMAVWFAQKKKK+ 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 RKEQIREQIELGILSYGAGVASLPLINVIAHNPGSVI------SATPIYKGPC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 ------GTGSRGSYAAPSPFTS--SHNSGTLFLRPQSPANFLGSGSGSDFVYSPS 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 OPPAPPPNAFVEIVSS-----STGIIIAVGI-FAFIPSFLYKLLOWYNRKSKNKK 57
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APPLICANT: Le Rose Thomas J
APPLICANT: Le Rovalic David K
APPLICANT: Avalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38 -21(5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OP SEQ ID NOS: 285684
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Best Local Similarity 25.7%; Pred. No. 11;
Matches 38; Conservative 18; Mismatches 45; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 756,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_23247C.1.pep
US-10-424-599-200688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.2%; Score 80.5; DB 15; Best Local Similarity 25.7%; Pred. No. 11; Matches 38; Conservative 18; Mismatches 45;
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US-10-425-114-39701
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                                                                                                                                                                                                                                                                                               SEQ ID NO 200688
LENGTH: 756
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Broukharov, Andrey A.
APPLICANT: Broukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERRNCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 183058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 PPPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIREQI---ELGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.9%; Score 78.5; DB 16; Length 419; Best Local Similarity 23.0%; Pred. No. 8.3; Matches 32; Conservative 22; Mismatches 44; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Clone ID: PAT_MRT4530_80186C.1.pep
US-10-437-963-183058
Sequence 183058, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryza sativa
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                                                                                                                                                       Sequence 290480, Application US/10425115
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 29480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Green, Jack E
APPLICANT: Cao, Yongwel
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERRICE: 38-21(53313)8
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 4326
LENGTH: 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 PLINVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHDGR-NPDGSI 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.0%; Score 79.5; DB 17; Length 539; 35.6%; Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: MRT4577_28005C.1.pep
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US-10-425-114-43526
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     --- LLQITSGTAEEN 123
                                389 EPGGVSSSRSWFTYEELIQATNGFSAQN 416
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  105 T--GVPNSR-
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Best Local Similarity
Matches 21; Conserv
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ORGANISM: Zea mays
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slaters, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT PELLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 325
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239 PPPIAHLHAVKA------IMEMLWWYNNGYKVKMESERSNQGIMEEDSV 281
                                                      71 LSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQI------TSGTAEEN 123
                                                                                                          282 ISNGGREEEV----VVANGSGGGVGGT----ARSSGGGGGKVVQVLQRNFGEVQGILEQN 333
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) ORGANISM: Sphingomonas aromaticivorans
US-10-369-493-10884
                                                                                                                                                                                                                                                                                                                                                       Sequence 10884, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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RESULT 13 US-10-437-963-183058

Search completed: November 15, 2004, 15:01:30 Job time : 142 secs

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protein B0207.12 [
probable integral
protein-tyrosine k
hypothetical prote
SLN1 protein - yea
hypothetical prote
hypothetical prote
probable gluconate
ND3 intron protein
hypothetical protein
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GenCore version.5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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phosphoribosylaminoimidazole carboxylase (BC 4.1.1.21) catalytic chain - Aquifex aeolic

217

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RESULT 2 D70401

93 VISATPIYKGPCTGVPNSRLLQITSGTABENTRILNHD

C;Species: Aquifex aeolicus C;Date: OB-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004 C;Accession: D70401 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,

D.B., 9

Nature 392, 353-358, 1998

A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A; Reference number: A70300; MUID:98196666; PMID:9537320

A; Reference number: A70300; MUID:98196666; PMID:9537320

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-167 < AQC>

A; Cross-references: UNIPROT:067239; GB:AE000727; NID:92983623; PIDN:AAC07201.1; PID:9298

A; Experimental source: strain VP5

11.5 9.9 185 2 AH3477 tryptophan- 12 70.5 9.8 431 2 A72394 developmental 2 70.5 9.8 415 2 A72394 developmental 2 70.5 9.8 415 2 B89391 hypothetical 3 70.5 9.8 1588 2 73860 probable tryptophetical 3 70.5 9.8 1588 2 73860 probable tryptophetical 3 70.5 9.8 7 322 2 861227 probable tryptophetical 3 70.5 9.7 708 2 P71110 propable tryptophetical 3 80.5 9.7 708 2 P71110 propable tryptophetical 3 80.5 9.7 708 2 P71110 propable tryptophetical 4 80.5 9.7 881 2 732074 propable tryptophetical 4 80.5 9.7 881 2 732074 propable tryptophetical 4 80.5 9.7 881 2 732074 propable tryptophetical 4 80.5 9.6 50.1 1192 2 732074 propable tryptophetical 4 80.5 9.6 50.1 1192 2 732074 propable tryptophetical 6 9.6 50.1 1192 2 732074 propable tryptophetical 7 9.7 1100404 2 7 1 110040	tryptophan-tRNA li adenyloauccinate l hypothetical prote probable transcrip lipase A precursor flagellar basal bo hypothetical prote hypothetical prote phosphoribosylamin hypothetical prote phypothetical prote phypothetical prote proplamic sugar- cytochrome P450 2D conserved hypothet PTS system, mannit phosphotransferase	ALIGNMENTS Imported] - Staphylococcus aureus (strain N315) s aureus sence_revision 10-May-2001 #text_change 09-Jul-2004 Jchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu, Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Juencing of meticillin-resistant Stapylococcus aureus. S8; MUID:21311952; PMID:11418146 S7: Amilian N315 stain N315	ch 11.7%; Score 84; DB 2; Length 431; 1 Similarity 26.5%; Pred. No. 1.8; 26; Conservative 15; Mismatches 35; Indels 22; Gaps 2; 33 GIPAPIFSFLYKLLQWYNRKSKNXKRKEQIREQIELGLLSYGAGVASLPLIAVIAHNPGS 92 :
11.5 9.9 385 2 1 70.5 9.8 431 2 2 70.5 9.8 431 2 3 70.5 9.8 431 2 4 70 9.7 323 2 7 0 9.7 536 2 6 69.5 9.7 708 2 6 69.5 9.7 881 2 6 69.5 9.7 881 2 6 69.5 9.7 881 2 6 69.5 9.7 881 2 6 69.5 9.7 881 2 6 69.5 9.7 881 2 6 69.5 9.7 881 2 6 69.5 9.7 881 2 6 69.5 9.7 881 2 6 69.5 9.7 881 2 6 9.6 582 2 6 9 9.6 580 1 1 10 May-2001 #Bequence_real and the sequencing area to mamber: A89758; MUID: A MID:	AH3477 AH3477 A72294 BB3331 T38660 S61927 S61927 S61927 T1110 F71110 T12074 AH1934 AH1934 AD6691 B95045	ALIGNM - Staphy rision 10- I.; Baba ii, N.; Sa iwwara, N. of metici 21311952; 5	Score 84 Pred. No .5; Misma KSKNKKKE KSKNKKKE : : :
11.5 9.9 385 1 70.5 9.8 443 1 70.5 9.8 445 2 70.5 9.8 1588 4 70 9.7 323 7 0 9.7 328 6 69.5 9.7 368 6 69.5 9.7 368 6 69.5 9.7 368 6 69.5 9.7 1119 6 69.5 9.7 1119 6 69.5 9.6 502 6 69.5 9.6 502 2 69.9 9.6 502 3 69.9 9.6 502 4 69.9 9.6 502 5 69.9 9.6 502 5 69.9 9.6 502 5 69.9 9.6 502 6 9.6 502 7 1119 6 9.6 502 7 1019 7 10	00000000000000000	red] ana, ama, ast ast JID: JID: ase	74; 54; 1 1 VYNE VYTE
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THE THE COUNTRY OF THE CALL OF	O H W W W W V & W O H W M W W	RESULT 1 C89979 adenylosuccinate 1 C; Species: Staphyl C; Date: 10. May 200 C; Accession: C8997 R; Kuxoda, M.; Ohta M. A.; Malutani-U C; Shiba; T.; Ha Lancet 357, 1225-1 A; Title: Whole gen A; Accession: C8997 A; Accession: C8997 A; Accession: C8997 A; Accession: C8997 A; Cross-references A; Accession: C8997 A; Cross-references A; Accession: C8997 A; Cross-references C; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Superfamily: fum	Ouery Match Best Local Simil Matches 26; C 33 GIFA 142 GVHA

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C;Species: Listeria innocua
C;Species: Listeria innocua
C;Accession: AH1659
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke:
C;Acossion: AH1659
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke:
C;Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Bntian, K.D.; Fsthi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland.
A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland.
A;Title: Comparative genomics of Listeria species.
A;Accession: AH1699
A;Accession: AH1699
A;Accession: AH169
A;Rostulus: L.32 - CGLA
A;Residuss: L.32 - CGLA
A;Residuss: L.32 - CGLA
A;Residuss: L.32 - CGLA
A;Experimental source: strain Clip11262
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C; Date: 11-Mar-2000 #sequence_revision 11-Mar-2000 #text_change 09-Jul-2004
C; Accession: A31351
R; Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillii
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre.
Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyman A; Reference number: A81250; MUID:20150912; PMID:10688204
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A;Cross-references: UNIPROT:Q8Y5M5; GB:NC_003210; PIDN:CAD00110.1; PID:g16411502; GSPDB
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                                                                                                                                                                                                                                                                                                                                                 38; Gaps
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                                                                                                                                                                                                                                                           DB 2; Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 392;
                                                                                                                                                                                                                                                       Ouery Match 10.8%; Score 78; DB 2; Length 391
Best Local Similarity 28.3%; Pred. No. 6.3;
Matches 30; Conservative 14; Mismatches 24; Indels
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                                            A,Experimental source: strain EGD-e
C,Generics:
A,Gene: ftsZ
C,Superfamily: cell division protein ftsZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: ftsZ
C,Superfamily: cell division protein ftsZ
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Matches 30, Conservative
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A; Residues: 1-339 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: preliminary
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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1328
C;Accession: AH1328
C;Accession: AH1328
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Residues: 1-391 cGLA>
A;Residues: 1-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cjaccession: A75507
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                        A,Gene: purB
C;Superfamily: phosphoribosylaminoimidazole carboxylase catalytic chain; phosphoribosyls
C;Keywords: carbon-carbon lyase; carboxy-lyase; purine nuclectide biosynthesis
F;3-136/Domain: phosphoribosylaminoimidazole carboxylase catalytic chain homology <PCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell-division initiation protein FtsZ homolog ftsZ [imported] - Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                  5 HSIVQPPAPPPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNK--KRKEQI
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                                                                                                                                                                                                                                                           DB 2; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 10.8%; Score 78; DB 2; Length 255; Similarity 27.3%; Pred. No. 3.9; 30; Conservative 14; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                            28, Indels
                                                                                                                                                                                                                                                       11.5%; Score 83; DB 2;
33.8%; Pred. No. 0.77;
tive 15; Mismatches
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                                                                                                                                                                                                                                         Query Match
Best Local Similarity 33.84
Matches 23, Conservative
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Best Local Similarity
Matches 30; Conserv
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C, Genetice:
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A;Status; preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1477 <STE>
A;Cross-references: UNIPROT:Q25197; EMBL:M64612; NID:g858746; PID:g858747; PIDN:AAA6820
A;Experimental source: adult polyp
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Residues: 1-427 <OLI>
; Cross-references: UNIPROT: P25555; EMBL: X59720; NID: g1907116; PIDN: CAA42348.1; PID: e26
                                                                                                                                                                                                                                                                                                                                                                        R;Steele, R.E.; Mai, N.H.; Lieu, P.; Shenk, M.A.
submitted to the EMBL Data Library, May 1995
A;Description: An insulin-like receptor gene is expressed in dividing epithelial cells
A;Reference number: 218954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rioliver, S.G.; Anwar, R.; Brown, A.; Gent, M.E.; Indge, K.J.; James, C.M.; Stateva, submitted to the Protein Sequence Database, March 1992
A;Reference number: S19337
A;Accession: S19338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...; | :: | :: | ...
                                                        57 KRKEQIREQIELGILSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQIT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 VEIVSSSTGIIIAVGIPAFIFSFLYKLL ------CMYNRK-----SKNK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein YCL011c - yeast (Saccharomyces cerevisiae)
C.Species: Saccharomyces cérevisiae
C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-2004
2.Accession: S19338
                                                                                                                                                                                                                                                                                                                                             C,Species: Hydra vulgaris
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: nucleus
F;123-188/Domain: ribonucleoprotein repeat homology «RRM1»
F;220-286/Domain: ribonucleoprotein repeat homology «RRM3»
F;350-416/Domain: ribonucleoprotein repeat homology «RRM3»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: HTK7
C;Superfamily: insulin receptor; protein kinase homology
                                                                                                                                                                                                                                                                                                       protein-tyrosine kinase - Hydra vulgaris
N;Alternate names: insulin-like receptor protein
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C; Superfamily: ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.6%; Score 76; DB
Best Local Similarity 20.9%; Pred. No. 45;
Matches 28; Conservative 25; Mismatches
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A;Cross-references: SGD:S0000517; MIPS:YCL011c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1042 EKIELIR---ELGQGSFGM---
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23.5%;
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                        29 IIAVGIFAFIFS.
                                                                                                                                                                          276 VVIVFA 281
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Best Local Similarity
                                                                                                                          82 LLNVIA 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein B0207.12 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: C87791
R;anonymous, The C. elegans Sequencing Consortium.
S;cience 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Note: see websites genome, wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
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| Experimental Bource: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Molecule type: DNA
A; Residuces: 1-654 <STO>
A; Cross-references: GB: Chr I; PIDN: AAB52465.1; PID: 91943811; GSPDB: GN00019; CESP: B0207.1
A; Note: Similar to ligand-gated lonic channel
C; Genetics:
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A; Reference number: 221574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
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                                                                                                                                                                                                                61 WILDKEKNIILONOEALKOPKLLSIISLDKIRDELEFEGRFYA-----VKIIAHNEK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 WYNRKSKN-----KKRK-----EQIREQIELGLLSYGAGVASLPLLNVIAHNPG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable integral membrane transport protein - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 PPNAFVEIVSSSTGIIIAVGIFAFIFSFL--YKLLQWYNRKS---KNKGRKEQI----
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                 92 SVISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHDGRNPDGSINV 140
                                                                                                                                                                                                                                                                                                                  Length 654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.6%; Score 76; DB 2; Length 298; Best Local Similarity 34.8%; Pred. No. 7.3; Matches 23; Conservative 14; Mismatches 21; Indels
                                                                         ch 10.8%; Score 77.5; DB 2; Length 3. Similarity 28.4%; Pred. No. 6; 31; Conservative 14; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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A;Molecule type: DNA
A;Residues: 1-298 <SEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.8%; Score 77.5; I
29.9%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 29.9
Matches 26; Conservative
                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T36900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: T36900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Gene: B0207.12
A, Map position: 1
                        A, Gene: Cj0793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
C, Genetica
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Gaps

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Cross-references: UNIPROT:Q99RV2; GB:BA000018; PID:g13702121; PIDN:BAB43413.1; GSPDB:<
    Experimental source: strain N315
                                                                                                                                                                                                       A/Reaidues: 1-399 <KAN>
A/Cross-references: UNIPROT:P74550; EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA186
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C/Genetics:
  ; Shimpo, 8.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
                             DNA Res. 3, 109-136, 1996
A,Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RiOliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999
A/Reference number: Z21614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CjAccession: D90031
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Inoue, R.; Kaito, C.; Sekimizu, M.; A.; Mizutani-Ui, Y.; Kobayashi, N.; Bawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A,Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pothetical protein SA2112 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Staphylococcus aureus
Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 APPPNAFVEIVS--SSTGIIIAVG-----IFAFIFSFLYKLLQWYNRKSKNKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Species: Streptomyces coelicolor
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C.Accession: T36781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 IVSSSTGIIIAVGIFAFIFSFLYKLL----QWYNRKSKNKKKEQIREQIELGLLSYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Superfamily: Bacillus subtilis sodium-dependent transporter yocs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: 874322; WUID:97061201; PMID:8905231
A;Accession: 876745
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%; Score 74.5; DB 2; Length 305; 30.3%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable gluconate permease - Streptomyces coelicolor (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 OLLDAIAIGOITPGPLFTTATFIGYLLAGNPGAIAATVGIF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 QIREQIELGLLSYGAGVASLPLLN-VIAHNPGSVISATPIY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                10.4%; Score 75; DB 23.8%; Pred. No. 13; ive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 GVASLPL-LNVIAHNPGSVISATPIYKGP 103
                                                                                                                                                                                                                                                                                                                                                                             Superfamily: chromate resistance protein A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 23.8*
Matches 24, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Status: preliminary
A Molecule type: DNA
A, Residues: 1-305 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: D90031
                                                                                                                                                                                                                                                                                                                                               A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlAccession: T36781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .lecule type: DNA
.sidues: 1-1220 <CHU>
.oss_references: UNIPROT:P39928; GB:Z47047; EMBL:Z38059; NID:g603997; PID:g763199; MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keywords: autophosphorylation; phosphoprotein; signal transduction; transmembrane prod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: 876745
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asemizu, B.; Nakamura, Y.; Miyajima, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ġ
                                                                                                                247
                                                                                                                                                                                                          :|| : | : | : | : | 248 ADVELDFNGFSRĞFGS-----VIYPTEDEMIRAIDTFNGM---EVEGRVLEVREGRFNKR 299
                                                                                                                                                                   64 BQIELGLLSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSGTAEEN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 VSQPESVFLSPA-----TKLAKIITGTVIAIGVFVILLTL--PLAHW------AVQP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NiAlternate names: protein YIL147c
CiSpecies: Saccharomyces cerevisiae
CiDate: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
CiAccession: S48387; S48888
RiChurcher, C.
                                                                                            4 RHSIVOPPAPPPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLOWYNRKSKNKKRKEQIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 QIREQIELGLLSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTG--VPNSRLLQITSG
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        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ta, I.M.; Varshavsky, A.
ence 262, 566-569, 1993
litle: A yeast protein similar to bacterial two-component regulators
eference number: 8488888; MUID:94024010; PMID:8211183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
10.5%; Score 75.5; DB 2; Length 1220;
Best Local Similarity 23.3%; Pred. No. 41;
Matches 31; Conservative 22; Mismatches 53; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:24-40/Domain: transmembrane #status predicted <TM1>
F:334-350/Domain: transmembrane #status predicted <TM2>
F:1090-1206/Domain: response regulator homology <RRH>
F:1144/Binding site: phosphate (Asp) (covalent) #status predicted
18; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ubmitted to the EMBL Data Library, September 1994 Reference number: S48310 Accession: S48387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: SGD:SLN1; YPD2
Cross-references: SGD:S0001409; MIPS:YIL147c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein - yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 IVRLOKATELITEGRGLR---
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31, Conservative
                                                                                                                                                                                                                                                                                    124 TRILINHDGRNPD 135
                                                                                                                                                                                                                                                                                                                           KNNDRYNQRRED 311
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A;Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues: 1-1220 <OTA>
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Matches
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Residues: 1-359 <OLI>
Cross-references: UNIPROT:Q8CK22; EMBL:AL096811; PIDN:CAB46778.1; GSPDB:GN00070; SCOED
Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                 | :| || || :: | :: | :: |: || :| || 68 HGLV-PPHPGPLVAIDAVDANLGVTLALGVLIAIPTVIIAGPVFSKYAARWVDVPAPDRM 126
                                                                                                                                                                                                                                                                                                                                                           5 HSIVOPPAPPPNAFVEIVSSSTGIIIAVGIPAFIFS-----FLYKLLQWYNRKSKNKK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 IPORASERLD-KRPSFGATLATILLPVVLMLLKALVDIIIDDPDNVVQRT 175
                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 RKEQIREQIELGLLSYGAGVASL------PLLNVIAHNPGSVISAT 97
                                                                                                                                                                                                                                                 Length 359;
                                                                                                                                                                                                                                                                                                        38; Indels
                                                                                                                                                                                                                                                 DB 2;
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                              ; Score 74.5; DI
; Pred. No. 13;
30; Mismatches
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 20.9%;
Matches 23; Conservative 3
                                                                                                                                                              A, Gene: SCOEDB: SCI30A.01
C, Superfamily: D-serine permease
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03 intron protein - Podospora anserina mitochondrion Species: mitochondrion Podospora anserina Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004

Accession: 805654
Cummings, D.J.; Domenico, J.M.
Mol. Biol. 204, 815-819, 1988
Accession: 805654
Scatus: not compared with conceptual translation
Molecule type: DNA
Residues: 1-413 cCUM
Cross-references: UNIPROT:P15563

A, Genome: mitochondrion A, Genetic code: SGC3 C, Keywords: mitochondrion

Query Match Best Local Similarity 23.99 Matches 33; Conservative

22 VSSSTGIIIAVGIFAFIFSFLY------KLLQWYNRKSKNKKRK---EQIREQ 65 ò 셤

20; Mismatches

28;

DB 2; Length 433; 57; Indels

ENTRILNHDGRNPDGSIN 139

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----ISYQAKIPSNSIN 130

Search completed: November 15, 2004, 14:58:22 Job time : 45 sec8

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GenCore version 5.1.6
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- protein search, using sw model OM protein Run on:

November 15, 2004, 14:32:21 ; Search time 195 Seconds (without alignments) 413.089 Million cell updates/sec

US-09-943-002-14 720 1 MGRHSIVQPPAPPPNAFVE......EBNTRILAHDGRNPDGSINV 140 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181

1825181 segs, 575374646 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot sprot:*
2: uniprot_trembl:* UniProt 02:* Датараве :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES	Description	Q918v6 baboon reov							Q8dgc1	•	022040							Q9rwx1 deinococcus	Q8y5m5 listeria mo	Q71xy1	4		O9ppc6 campylobact	Q17369 caenorhabdi	Q95q97 caenorhabdi	Q833i4 enterococcu	Q9ffw5 arabidopsis	Q8rf10 fusobacteri	_	Bac84718 oryza sat	ASARA BLIANTOMOCO
E S	Ð	0918V6	Q7QPH4	Q6G825	Q6GFE9	6XS660	Q7A0G9	Q7A4Q3	QBDGC1	PUR6_AQUAE	022040	969010	Q8CRT6	Q6F2A9	080115	Q8LP72	089909	Q9RWX1	Q8Y5M5	Q71XY1	AAT0483	Q929Y5	D9PPC6	017369	095097	Q833I4	Q9FFWS	QBRF10	06YT74	BAC84718	979X90
	DB	5	N	C3	~	~	~	~	N	-	N	~	~	~	ď	~	N	~	~	~	~	~	~	~	~	~	~	N	~	~	^
	ouery Match Length	140	806	431	431	431	431	431	574		636	734	431	443	1491	633	664	255	391	391	391	392	339	430	430	172	681	187	280	280	298
a	Query Match	100.0	11.9	11.7	11.7	11.7	11.7	11.7	11.7	11.5	11.5	11.4	•	11.0	11.0	11.0	11.0	10.8	10.8	10.8	10.8	٠	10.8	٠	10.8	10.7		•	10.6	10.6	10.6
	Score	720	85.5	84	84	84	84	84	84	m	82.5	82	.80.5	79.5	79.5	79	79	78	78	78	78	78	77.5	77.5	77.5	77	76.5	92	16	92	76
	Result No.	-	73	m	4	ហ	φ	7	80	σ	10	, 11	12	13	14	15	. 16	17	18	19	20	21	22	23	24	25	56	27	28	53	90

Q7m857 wolinella s Q25197 hydra atten	P25555 saccharomyc P39928 saccharomyc P74550 synechocyst	Q7rg91 plasmodium Q72r7 bacillus ce Aas43502 bacillus	Q821z3 chlamydophi Q8pz47 methanosarc O9v438 homo sapien		Q99rv2 stapnylococ
Q7M857 HTK7 HYDAT	GBP2_YBAST SLN1_YEAST P74550	Q7RG91 Q72ZR7 AAS43502	LPXB CHLCV Q8PZ47 09Y438	Q6G629 Q8NV71	Q99RV2
77	448	0 0 0	- 70 70	00	~
765	427 1220 399	481 508 508	626 848 892	305	305
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328	4.7.0 6.00	2 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 0 H 2	4 4 E 4	45

ALIGNMENTS

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61 QIREQIBLGLLSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTGVPNSKLLQITSGTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 QIREQIELGLLSYGAGVASLPLLMVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSGTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGQRHSIVQPPAPPPNAFVEIVSSSTGIIIAVGIPAFIFSFLYKLLQWYNRKSKONKKRKE 60
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                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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SEGUENCE FROM N.A.
STRAINSWE C6;
Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 720; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.7e-63;
Matches 140; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLP 41 11524 13944.
Giardia lamblia ATCC 50803.
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
NCBI TaxID=184922;
                                                                                                                                                                                         SEQUENCE FROM N.A.
Dawe S., Duncan R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Shou J., Chen Z., Duncan R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF406781, AAL01373.1, -
SEQUENCE 140 AA; 15222 MW; B02BDF37E6CE6075 CRC64;
                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Membrane fusion protein p15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                        Baboon reovirus.
Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
NCBI_TaxID=75888;
                               140 AA
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                               PRT;
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                               PRELIMINARY;
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                             Q918V6
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RESULT 1
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                0918V6
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SEQUENCE FROM N.A.
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0995X9
1D 0995X
DT 01-91
DT 01-01
DT 01-M
DB Meme
OS Stap
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Q6GFE9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 GAGVASLPLLNVIAHNPGSVISATPIYKGPCTGV------PNSRLLQ-----ITSGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441 GHGVLATPVLTL----SSIIGSGSI---RWTGVSISNDITSANSNRLEAGTNGDMTPGS 492
                                                                                                                                                                                                                                                                                                                                                                                                                     PPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIREGGLLSY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Buright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
Ormond D., Quall M.A., Rabbinowitsch B., Rutherford K., Sanders M.,
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Complete genomes of two clinical Staphylococcus aureus strains:
"Complete genomes of two clinical Staphylococcus aureus strains:
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
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                                                                                                                       preliminary data.

EMBL; ARCE0100169; EAA36911.1; -.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0006155; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001965; Znf PHD.
Pfam; PP00628; PHD; 1.

SEQUENCE 806 AA; 90537 MW; CD93E0653EF38DB9 CRC64;
Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                    / Match 11.9%; Score 85.5; DB 2; Length 806; Local Similarity 24.5%; Pred. No. 18; les 35; Conservative 21; Mismatches 44; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Adenylosuccinate lyase (EC 4.3.2.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus subsp. aureus MSSA476.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003031; D_crystallin.
InterPro; IPR003042; Fumarate lyase.
InterPro; IPR008948; L-Aspartase-like.
InterPro; IPR004769; Pur lyase.
Pfam; PF00206; Lyase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 AE------ENTRIL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493 ASAANGPHASMRQTNSIKNTKVI 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Andrew M. T. G., Feil B. J., Lindsay J. A., Peacock S. J., Day N. P. J.,

Holden M. T. G., Feil B. J., Lindsay J. A., Peacock S. J., Day N. P. J.,

Enright M. C., Foster T. J., Moore C. B., Hurst L., Atkin R., Barron A.,

A Bason N. Benley S. D., Chillingworth C., Chillingworth T.,

Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,

A James K. D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

A Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K., Sanders M.,

Sharp S., Simmonds M., Stevens K., Whitchead S., Barrell B.G.,

Spratt B.G., Parkhill J.,

R. Sharp S., Candols S. L. Barrell B.G.,

E. M. Complete genomes of two clinical Staphylococcus aureus strains:

evidence for the rapid evolution of virulence and drug resistance.",

Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

R. EMBL, BSK71856, GAG40985.1, -.

R. InterPro; IPR003031; D. Crystallin.

InterPro; IPR003031; Fumarate. Lyase.

R. InterPro; IPR003648; L. Marate. Lyase.

InterPro; IPR008648; L. Marate. Lyase.

InterPro; IPR008648; L. Marate. Lyase.
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33 GIFAFIFSFLYKLLOWYNRKSKNKKRKROIREQIELGLLSYGAGVASLPLLNVIAHNPGS
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                                                                                                                                             93 VISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHD 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
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Name-purB, OrderedLocusNames-SAV1908;
Staphylococcus aureus (strain Mu50 / ATCC 700699)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus subsp. aureus MRSA252.
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                   431 AA
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PROSITB; PS00163; FUMARATE_LYASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Pfam; PP00206; Lyase 1; 1.
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PRINTS; PR00149; FUMRATELYASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=purB; ORFNames=SAR2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 27, (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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HSSP;

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142 GVHAEPTTFGVKMALWYTEMORNLORFKOVREBIBVGKMSGAVG------TPANIPPE 193
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                                                                                                                                                                                                                                                                                                                                                                                   22; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21311952; PubMed=11418146; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Curoda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Gyuchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Mateumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                          Query Match 11.7%; Score 84; DB 2; Length 431; Best Local Similarity 26.5%; Pred. No. 12; Matches 26; Conservative 15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%; Score 84; DB 2; Length 431; 26.5%; Pred. No. 12;
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                                                                                                                               TIGRFAWS; TIGR00928; purB; 1.
PROSITE; PS00163; FUMARARE LYASES; 1.
Complete proteome; Lyase.
SEQUENCE 431 AA; 49603 MW; 493F79CBE814B9E5 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=purB; OrderedioousNames=SA1724;
Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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EMBL, AP003135; BAB42994.1; -...
EMBL, AP003135; BAB42994.1; -...
INCEPPO; IPR003031; D_crystallin.
INCEPPO; IPR003031; D_crystallin.
INCEPPO; IPR003051; Funarate lyase.
INCEPPO; IPR003051; Funarate lyase.
INCEPPO; IPR004949; Pur lyase.
Pfam; PR00145; DGRZTALLIN.
PRINTS; PR00145; PURRATELXASE.
TIGREAMS; TIGR00928; PURE; 1.
PR053TE; PS00163; FUMRATELXASE.
COMPLECE PFOCEOME; Lyase.
SEQUENCE 431 AA; 49603 MW; 493F79CBE.
InterPro; IPR004769; Pur lyase.
Pfam: PF00206; Lyase 1: 1.
                                    Pfam; PF00206; Lyase 1; 1.
PRINTS; PR00145; DCRYSTALLIN.
PRINTS; PR00149; FUMRATELYASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                           SEQUENCE FROM N.A.
STRAIN=MUSO / ATCC 700699;
STRAIN=MUSO / ATCC 700699;
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Mateumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani Ui Y., Takahashi N.K., Sawamo T., Inoue R.-I., Kaito C.,
Sekimizu K., Hizakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus.";
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MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Badai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
acquired MRSA.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO: 0004018; F: adenylosuccinate lyase activity; IEA. GO; GO: 0016829; F: lyase activity; IEA. GO; GO: 0016829; F: lyase activity; IEA. GO; GO: 0016825; F: purine ribonuclectide biosynthesis; IEA. InterPro; IPR003031; D_crystallin.
InterPro; IPR003031; D_marate lyase.
InterPro; IPR008848; L-Aspartase-like.
InterPro; IPR00499; Pur lyase.
PEMINTS; PR00145; DCRYSTALLIN.
PRINTS; PR00149; FUWRATELYASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 84; DB 2; Length 431; 
; Pred. No. 12; 
15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49603 MW; 493F79CBE814B9E5 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Bacteria, Firmicutes, Bacillales, Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431 AA
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EMBL, AP004828; BAB95714.1;

GO; 00106129; F; lyase activity; IEA.

InterPro; IPR003031; D_crystallin.

InterPro; IPR000362; Fumarate lyase.

InterPro; IPR008948; L-Aspartase-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGR00928; purB; 1.
PROSTIE; PSOILG3; FUMARATE_LYASES; 1.
PROMIDLE PROCEOMS; LYASE:
SEQUENCE 431 AA; 49603 MW; 493F790
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EMBL; AP003363; BABS8070.1; -.
PIR; C89979; C89979.
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26.5%;
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                             NCBI_TaxID=158878;
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07A0G9;
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Matches
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"The complete genome of the hyperthermophilic bacterium Aquifex
                                                            Nature 392:353-358(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=SSSD1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Makamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Natanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kaneko T., Sato S., Ikeuchi M., Matanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Mateumoto M., Mateumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Importation S., Sugimoto M., Takeucho C., Sugimoto M., Takeuchi C., Takeucho S., Sugimoto M., Takeucho C., Sugimoto M., Takeuchi C., Takeucho S., Sugimoto M., Takeuchi S., Importation S., Sugimoto M., Takeuchi C., Takeucho S., Sugimoto M., Takeuchi S., Takeuchi S., Takeuchi S., Sugimoto M., Takeuchi S., Takeuchi S., Sugimoto M., Takeuchi S., Sugimoto S., Sugimoto M., Sugimoto M., Takeuchi S., Sugimoto S., Su
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 11.7%; Score 84; DB 2; Length 574; 1 Similarity 27.6%; Pred. No. 17; 24; Conservative 20; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Last sequence update).
01-OCT-2004 (Rel. 45, Last annotation update)
hosphoribosylaminodinidazole carboxylase catalytic subunit (RC 4.1.1.21) (AIR carboxylase) (AIRC).
Name=purE; OrderedLocusNames=AQ_1178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Aquificae, Aquificales, Aquificaceae, Aquifex.
                                                                                                                                                                                                                                                                                 Synechococcus elongatus (Thermosynechococcus elongatus) Bacteria; Cyanobacteria, Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome, Transmembrane, Transport.
SEQUENCE 574 AA; 64027 MW; 3A478A3F80FB4BBD CRC64;
                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                      574 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 ISATPIYKGPCTGVPNSRLLQITSGTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :: :: | | :: | | | 118 LALIALFPGSRMGVELAAIILIYTGMA 144
                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22225144; PubMed=12240834;
                                                                                                                                                                                                                                transporter permease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
01-OCT-2004 (Rel. 45, Last ann
                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                          OrderedLocusNames=t112397;
                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUR6_AQUAE
067239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-VP5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
                                                                                   QBDGC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUR6_AQUAB
                               RESULT 8
OBDGC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropasan Bioinformatics Institute. There are no restrictions on its twee by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 YSIVQMPAGIPVATVAIGNATNAGLLAVRILSIKYPBYAKKLDBYTEKLKBKVAKMNBEL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 HSIVQPPAPPPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNK--KRKEQI
FUNCTION: This subunit can alone transform AIR to CAIR, but in association with purK, which possesses an ArPase activity, an arrayme complex is produced which is capable of converting AIR to CAIR efficiently under physiological condition (By similarity). CATALYTIC ACTIVITY: 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-exboxylate = 5-amino-1-(5-phospho-D-ribosyl)imidazole + CO(2). PATHWAY: De novo purine biosynthesis; sixth step.
SUBUNIT: Homocctamer (By similarity).
SIMILARITY: TO OTHER BACTERIAL PURE, ALSO TO AIR CARBOXYLASE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating blology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome, Decarboxylase, Lyase, Purine biosynthesis. SEQUENCE 167 AA, 18037 MM, 99A62BB6000F50F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.5%; Score 83; DB 1; Length 167
Best Local Similarity 33.8%; Pred. No. 5;
Matches 23; Conservative 15; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minx M.;
Submitted (DEC-1995) to the BMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2004 (TrEMBLrel. 26, Last sequence update) 01-WAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein SSSD1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.5%; Score 83; 33.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR000031; AIR carboxyl.
Pfam; PF00731; AIRC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD002193; AIR_carboxyl; 1.
TIGRFAMB; TIGR01162; purE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000727; AAC07201.1; -. PIR; D70401; D70401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    investigating biology. The C
Science 282:2012-2018(1998).
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11.2%; Score 80.5; DB 2; Length 431; 34.0%; Pred. No. 27; ive 13; Mismatches 19; Indel8
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                         11.4%; Score 82; DB 2; Length 734; 26.9%; Pred. No. 35; tive 15; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0004018; F:adenylosuccinate lyase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0009152; P:purine ribonucleotide biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49591 MW; 08D770CAB109B72A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adenyloguccinate lyase.
OrderedLocushames=SRIS3;
Staphylococcus epidermidis.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            443 AA
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InterPro; IPR000362; Fumarate_lyase.
InterPro; IPR008948; L-Aspartase-like.
InterPro; IPR004769; Pur_lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIGREAMS; TIGRO0928; purB; 1.
PROSITE; PS00163; FUMARATE LYASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00145; DCRYSTALLIN.
PRINTS; PR00149; FUMRATELYASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 23, (TrEMBLrel. 23, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 28, (TremBLrel. 28, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 34.08
Matches 17; Conservative
                                   Query Match
Best Local Similarity 26.9
Matches 35, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome; Lyase. SEQUENCE 431 AA; 49591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                              113 LQITSGTAEE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  711 IOKTHATODE 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=ATCC 12228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC.12228
PubMed=12950922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O6F2A9;
01-OCT-2004 (
01-OCT-2004 (
01-OCT-2004 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8CRT6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6F2A9
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Q6F2A9
ID Q6F2A
AC Q6F2A
DT 01-OC
DT 01-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPSEPSNALRYGIADNVDLPIFMLAAVFGLLFCFACGLFAWRCFHNKNKKSKRRKSRSNS 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 --IREQIELGLLSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     529 TPSKTYODYGRFTYGDGSSS-----SOPG----TETYY----EPSLRLLD---- 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPAPPNAPVEIVSSSTG--IIIAVGIFAFIFSFLYKLLQW---YNRKSKNKKRKEQ--- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43; Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 636;
                                   Waterston R.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                   Wilson R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71728 MW; 2894A1E7428C0793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    734 734 734 734 734 AA09AFD311EAB054 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                $; Score 82.5; DB
$; Pred. No. 27;
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=agCG54493; ORFNames=ENSANGG00000008214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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EMBL, AAAB01008960, EAA11826.1;
Interpro; IPR001611; LRR.
Interpro; IPR007092; LRR.SDS22.
Interpro; IPR003591; LRR.Eyp.
Pfam; PF00560; LRR; 10.
                                                                                                                                                                                                                                                                                                                                      HSSP, P56276; 1FHG.
WormPep; SSD1.1; CE29458.
InterPro; 1PR001361; PN_III.
InterPro; IPR001359; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR003598; IG_C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE, PS50853; FN3; 1.
PROSITE; PS50835; IG_LIKE; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 11.5%;
1 Similarity 23.7%;
32; Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 AEENTRILNHDGRNP 134
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PIR, T16774; T16774.
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Pfam; PF00047; 19; 3.
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SMART; SM00409; IG; 3
SMART; SM00408; IGc2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al protein.
636 AA; 7
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Best Local Similarity
                                                                                                                                        SEQUENCE FROM N.A. STRAIN-Bristol N2;
STRAIN-Bristol N2;
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SEOUENCE 63
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RANGE SERVICE 
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                                                                                                                                          58 RKEQIREQIBLGLLSYGAGVASLPLLNVIAHNP-GSV----ISATPIYKGPCTGVPNSRL 112
                                               57
                                                                        8 VOPPAPPPNAFVEIVSSST-----GIIIAVGIFAFIFSFLYKLLQWYNRKSKNKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
"Genome-based analysis of virulence genes in a non-biofilm-forming
Staphylococcus epidermidis strain (ATCC 12228).";
MMOL. Microbiol. 49:1577-1593 (2003)
HSSP; Q9X010, 1C3C.
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69 GLLSYGAGVASLPLLNVIAHNPGSVISATPIY---KGPCTGVPNSRLLQITSGTAEB--- 122
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A dachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A rukuda X., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

HSSP: O08967; 1FFW.
   the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                           MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata X., Itoh M., Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata X., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; prepare in and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Surgains—CSTBL/GI, TISBUB=Head;
MEDLINE=CSTBL/GI,
MEDLINE=CSTBL/GI,
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
Mishia J., Nahi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.
"RIKEN Integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 79.5; DB 2; Length 1491; 27.2%; Pred. No. 1.4e+02; tive 22; Mismatches 42; Indels 35.
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GO; GO:0005856; C:Cytoskeleton; IEA.
GO; GO:0003779; F:actin binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003774; F:motor activity; IEA.
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InterPro, IPR011036; PH related
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PROSITE; PS50003; PH_DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000299; Band 4.1.
InterPro; IPR009065; FERM.
InterPro; IPR000857; MyTH4.
                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
                                                                60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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SMART; SM00139; MYTH4; 1.
SMART; SM00233; PH; 2.
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Pfam; PF00169; PH; 1.
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wes 37, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Matches
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
11brary, clone:4831441H15 product:hypothetical Serine-rich region/Band
4.1 family/PH domain profile/Core domain in kinesin and myosin
motors/Pleckstrin homology (PH) domain containing protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVEIVSSSTGIIIAVGIFAFIFSFLYKLL------QWYNRKSKNKKRKEQIREQ
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE-Head; WBDINES-110851; STREAT PANTOM CONSOCTION; RIKEN FANTOM CONSOCTION; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                           Birren B.W., Stange-Thomann N., Hafez N., DeCaprio D., Fisher Butler J., Elkins T., Kodira C.D., Major J., Wang S., Nicol R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knight T. Jr., Fournier G.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017263; AAT75357.1; -.
SEQUENCE 443 AA; 50263 MW; F0B9AF49504EBE19 CRC64;
                                                                                                                                                                                                                                                                                                                                                           Nusbaum C.,
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                              Bacteria, Firmicutes, Mollicutes, Entomoplasmatales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
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MEDLINE-9927923; PubMed-10349636;
Carninci P., Hayashizari Y.;
"High-efficiency full-length cDNA cloning.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.0%; Score 79.5; D
24.8%; Pred. No. 35;
tive 26; Mismatches
Chromosomal replication initiator protein. ORFNames=Mf1001;
                                                                                                                                   Entomoplasmataceae; Mesoplasma
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STRAIN=C57BL/6J; TISSUE=Head;
The FANTOM Consortium,
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                                                                   florum L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
tes 31; Conserv
                                                                                                                                                                  NCBI_TaxID=265311;
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=L1;
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                                                            Mesoplasma
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                                                                                                                                                                                                                                                  Receptor-like procein kinase.
Nicotiana tabacum (Common tobacco).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                           Tto N., Takabatake R., Seo S., Hiraga S., Mitsuhara I., Ohashi Y.;
"Induced expression of a temperature-sensitive leucine-rich repeat
Treceptor-like procein kinase game by hypersensitive cell death and
wounding in tobacco plant carrying the N resistance gene.";

Plant Cell Physiol. 43:266-274(2002).

Plant Cell Physiol. 43:266-274(2002).

RMD./ ABO73628; BAC07504.2;

RMD./ ABO73628; BAC07504.2;

RMD./ ABO73628; Proceeptor activity; IEA.

RMD./ GO:0004574; F:protein serine/threonine kinase activity; IEA.

RMD./ GO:0004877; P:receptor activity; IEA.

RMD./ GO:001640; F:transferase activity; IEA.

RMD./ GO:0016468; P:protein amino acid phosphorylation; IEA.

Theory. IPROLIBON; Kinase_like.
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PROSITE: PSSO011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
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                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                              633 AA
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nterpro; IPR000719; Prot kinase.
nterpro; IPR008271; Ser_thr_pkin_AS.
fam; PP00050; LRR; 6.
fam; PP00069; Pkinase; 1.
                                                                                                                                                                              PRT;
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MEDLINE=21914716; PubMed=11917080;
Ito N., Takabatake R., Seo S., Hir
--NTRILNHDGRNPDG 136
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